

4-31452A.ST25.txt
SEQUENCE LISTING

<110> Novartis AG

<120> Adenovirus particles with mutagenized fiber proteins

<130> 4-31452A

<160> 43

<170> PatentIn version 3.0

<210> 1

<211> 1746

<212> DNA

<213> Human adenovirus type 5

<220>

<221> CDS

<222> (1)..(1746)

<400> 1

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

09870203.053001

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

4-31452A.ST25.txt

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

285

9

300

9

320

10

335

10

350

11

365

11

380

12

SECRET

4-31452A.ST25.txt

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa
84

15

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac
32

16

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc
80

16

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca
28

17

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa
46

17

Tyr Ile Ala Gln Glu

580

<210> 2

<211> 581

<212> PRT

<213> Human adenovirus type 5

<400> 2

09070200-052001
T00250#00204860

4-31452A.ST25.txt

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
180 185 190

09870203 053001

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

09070203-053004

Tyr Ile Ala Gln Glu
580

<210> 3
<211> 1746
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)

<220>
<221> mutation
<222> (1222)..(1227)

<400> 3
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

09870203-053001
F00250-20204860

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12

48

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12

96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13

44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13

92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14

40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14

88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15

Tyr Ile Ala Gln Glu
580

<210> 5
<211> 1740
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted

<220>
<221> CDS
<222> (1)..(1740)

<400> 5
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg
76

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg
24

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act
72

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act
20

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca
68

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt
16

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag
64

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

4-31452A.ST25.txt

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
 12
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9
 60
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
 08
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
 56
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
 04
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
 52
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
 00

09070203 053001

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12

48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12

96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13

44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13

92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14

40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg 14

88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt 15

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

09370203.053001

Ala Gln Glu

<210> 7

<211> 1740

<212> DNA

<213> Artificial

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Combination of the mutant fiber encoded in Seq ID: #3 & 5

<220>

<221> CDS

<222> (1)..(1740)

<400> 7

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

180

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

195

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

210

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

225

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

245

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

260

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

275

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

| | | | | |
|---|-----|-----|-----|----|
| 385 | 390 | 395 | 400 | |
| ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag | | | | 12 |
| 48 | | | | |
| Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu | | | | |
| | 405 | 410 | 415 | |
| aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata | | | | 12 |
| 96 | | | | |
| Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile | | | | |
| | 420 | 425 | 430 | |
| ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga | | | | 13 |
| 44 | | | | |
| Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly | | | | |
| | 435 | 440 | 445 | |
| aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg | | | | 13 |
| 92 | | | | |
| Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val | | | | |
| | 450 | 455 | 460 | |
| cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat | | | | 14 |
| 40 | | | | |
| Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn | | | | |
| 465 | 470 | 475 | 480 | |
| gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg | | | | 14 |
| 88 | | | | |
| Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met | | | | |
| | 485 | 490 | 495 | |
| cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt | | | | 15 |
| 36 | | | | |
| Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser | | | | |

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15
84
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16
32
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa 17
40
Ala Gln Glu

<210> 8
<211> 579
<212> PRT
<213> Artificial

<400> 8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|-----|--|--|----|--|--|--|--|--|--|--|--|--|--|--|--|----|
| 1 | | | | | | | | | | | | | 5 | | | | | | | | | | | | | 10 | | | | | | | | | | | | | 15 |
| Tyr | Asp | Thr | Glu | Thr | Gly | Pro | Pro | Thr | Val | Pro | Phe | Leu | Thr | Pro | Pro | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | 20 | | | | | | | 25 | | | | 30 | | | | | | | | | | | | | | | | | | | | | | | | | |
| Phe | Val | Ser | Pro | Asn | Gly | Phe | Gln | Glu | Ser | Pro | Pro | Gly | Val | Leu | Ser | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 35 | | | | | | | 40 | | | | 45 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu | Arg | Leu | Ser | Glu | Pro | Leu | Val | Thr | Ser | Asn | Gly | Met | Leu | Ala | Leu | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 50 | | | | 55 | | | | | | | 60 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Met | Gly | Asn | Gly | Leu | Ser | Leu | Asp | Glu | Ala | Gly | Asn | Leu | Thr | Ser | | | | | | | | | | | | | | | | | | | | | | | | |
| 65 | | | | | | | 70 | | | | 75 | | | | | | | | | | | | 80 | | | | | | | | | | | | | | | | |
| Gln | Asn | Val | Thr | Thr | Val | Ser | Pro | Pro | Leu | Lys | Lys | Thr | Lys | Ser | Asn | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | 85 | | | | 90 | | | | 95 | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile | Asn | Leu | Glu | Ile | Ser | Ala | Pro | Leu | Thr | Val | Thr | Ser | Glu | Ala | Leu | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | 100 | | | | 105 | | | | 110 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Thr | Val | Ala | Ala | Ala | Ala | Pro | Leu | Met | Val | Ala | Gly | Asn | Thr | Leu | Thr | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | 115 | | | | 120 | | | | 125 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Met | Gln | Ser | Gln | Ala | Pro | Leu | Thr | Val | His | Asp | Ser | Lys | Leu | Ser | Ile | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | 130 | | | | 135 | | | | 140 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Thr | Gln | Gly | Pro | Leu | Thr | Val | Ser | Glu | Gly | Lys | Leu | Ala | Leu | Gln | | | | | | | | | | | | | | | | | | | | | | | | |
| 145 | | | | | | | 150 | | | | 155 | | | | | | | | | | | | 160 | | | | | | | | | | | | | | | | |
| Thr | Ser | Gly | Pro | Leu | Thr | Thr | Thr | Asp | Ser | Ser | Thr | Leu | Thr | Ile | Thr | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | 165 | | | | 170 | | | | 175 | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Ser | Pro | Pro | Leu | Thr | Thr | Ala | Thr | Gly | Ser | Leu | Gly | Ile | Asp | Leu | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | 180 | | | | 185 | | | | 190 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Glu | Pro | Ile | Tyr | Thr | Gln | Asn | Gly | Lys | Leu | Gly | Leu | Lys | Tyr | Gly | | | | | | | | | | | | | | | | | | | | | | | | |

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
485 490 495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac .2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att : 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

| | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag | | | | | | | | | | | | | | | | 12 |
| 48 | Leu | Trp | Thr | Thr | Pro | Ala | Pro | Ser | Pro | Asn | Cys | Arg | Leu | Asn | Ala | Glu |
| | | | | | 405 | | | | | 410 | | | | | 415 | |
| aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata | | | | | | | | | | | | | | | | 12 |
| 96 | Lys | Asp | Ala | Lys | Leu | Thr | Leu | Val | Leu | Thr | Lys | Cys | Gly | Ser | Gln | Ile |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct | | | | | | | | | | | | | | | | 13 |
| 44 | Leu | Ala | Thr | Val | Ser | Val | Leu | Ala | Lys | Gly | Ser | Leu | Ala | Pro | Ile | Ser |
| | | | 435 | | | | | 440 | | | | | 445 | | | |
| gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga | | | | | | | | | | | | | | | | 13 |
| 92 | Gly | Thr | Val | Gln | Ser | Ala | His | Leu | Ile | Ile | Arg | Phe | Asp | Glu | Asn | Gly |
| | 450 | | | | | | 455 | | | | 460 | | | | | |
| gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga | | | | | | | | | | | | | | | | 14 |
| 40 | Val | Leu | Leu | Asn | Asn | Ser | Phe | Leu | Asp | Pro | Glu | Tyr | Trp | Asn | Phe | Arg |
| | 465 | | | | | 470 | | | | | 475 | | | | 480 | |
| aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt | | | | | | | | | | | | | | | | 14 |
| 88 | Asn | Gly | Asp | Leu | Thr | Glu | Gly | Thr | Ala | Tyr | Thr | Asn | Ala | Val | Gly | Phe |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa | | | | | | | | | | | | | | | | 15 |
| 36 | Met | Pro | Asn | Leu | Ser | Ala | Tyr | Pro | Lys | Ser | His | Gly | Lys | Thr | Ala | Lys |

500

505

510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15
 84
 Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16
 32
 Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
 80
 Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545

550

555

560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
 28
 Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565

570

575

att gcc caa gaa taa 17
 43
 Ile Ala Gln Glu

580

<210> 10
 <211> 580
 <212> PRT
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<400> 10

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1 | | 5 | | | | | | | 10 | | | | | 15 | | |
| Tyr | Asp | Thr | Glu | Thr | Gly | Pro | Pro | Thr | Val | Pro | Phe | Leu | Thr | Pro | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Phe | Val | Ser | Pro | Asn | Gly | Phe | Gln | Glu | Ser | Pro | Pro | Gly | Val | Leu | Ser | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Arg | Leu | Ser | Glu | Pro | Leu | Val | Thr | Ser | Asn | Gly | Met | Leu | Ala | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Lys | Met | Gly | Asn | Gly | Leu | Ser | Leu | Asp | Glu | Ala | Gly | Asn | Leu | Thr | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Gln | Asn | Val | Thr | Thr | Val | Ser | Pro | Pro | Leu | Lys | Lys | Thr | Lys | Ser | Asn | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ile | Asn | Leu | Glu | Ile | Ser | Ala | Pro | Leu | Thr | Val | Thr | Ser | Glu | Ala | Leu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Thr | Val | Ala | Ala | Ala | Ala | Pro | Leu | Met | Val | Ala | Gly | Asn | Thr | Leu | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Met | Gln | Ser | Gln | Ala | Pro | Leu | Thr | Val | His | Asp | Ser | Lys | Leu | Ser | Ile | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ala | Thr | Gln | Gly | Pro | Leu | Thr | Val | Ser | Glu | Gly | Lys | Leu | Ala | Leu | Gln | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Thr | Ser | Gly | Pro | Leu | Thr | Thr | Thr | Asp | Ser | Ser | Thr | Leu | Thr | Ile | Thr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Ala | Ser | Pro | Pro | Leu | Thr | Thr | Ala | Thr | Gly | Ser | Leu | Gly | Ile | Asp | Leu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Lys | Glu | Pro | Ile | Tyr | Thr | Gln | Asn | Gly | Lys | Leu | Gly | Leu | Lys | Tyr | Gly | |

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

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385                               390                               395                               400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
      405                               410                               415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
      420                               425                               430

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
      435                               440                               445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
      450                               455                               460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
      465                               470                               480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
      485                               490                               495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
      500                               505                               510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
      515                               520                               525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
      530                               535                               540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
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Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
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Ile Ala Gln Glu

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580

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 <211> 1743
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<220>
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<220>
 <221> CDS
 <222> (1)..(1743)

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 1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1
 44
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1
 92
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
 76
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190

 aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
 24
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205

 gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
 72
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

 ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
 20
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

 gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
 68
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

 gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
 16
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

 agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
 64
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

| | | |
|---|-----|---------|
| ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 | | 9 |
| Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn | | |
| 290 | 295 | 300 |
| aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 | | 9 |
| Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu | | |
| 305 | 310 | 315 320 |
| gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 | | 10 |
| Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile | | |
| 325 | 330 | 335 |
| gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 | | 10 |
| Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro | | |
| 340 | 345 | 350 |
| aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04 | | 11 |
| Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp | | |
| 355 | 360 | 365 |
| tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 52 | | 11 |
| Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp | | |
| 370 | 375 | 380 |
| agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 00 | | 12 |
| Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr | | |

[illegible]

500

505

510

agc aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15
 84
 Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16
 32
 Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16
 80
 Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545

550

555

560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17
 28
 Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565

570

575

att gcc caa gaa taa 17
 43
 Ile Ala Gln Glu

580

<210> 12
 <211> 580
 <212> PRT
 <213> Artificial

<400> 12

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

| | | | | | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|----|--|--|--|
| 1 | 5 | | | | | | | | | | | | 10 | | | | 15 | | | |
| Tyr | Asp | Thr | Glu 20 | Thr | Gly | Pro | Pro | Thr 25 | Val | Pro | Phe | Leu | Thr 30 | Pro | Pro | | | | | |
| Phe | Val | Ser 35 | Pro | Asn | Gly | Phe | Gln 40 | Glu | Ser | Pro | Pro | Gly 45 | Val | Leu | Ser | | | | | |
| Leu | Arg 50 | Leu | Ser | Glu | Pro | Leu 55 | Val | Thr | Ser | Asn | Gly 60 | Met | Leu | Ala | Leu | | | | | |
| Lys 65 | Met | Gly | Asn | Gly | Leu 70 | Ser | Leu | Asp | Glu | Ala 75 | Gly | Asn | Leu | Thr | Ser 80 | | | | | |
| Gln | Asn | Val | Thr | Thr 85 | Val | Ser | Pro | Pro | Leu 90 | Lys | Lys | Thr | Lys | Ser 95 | Asn | | | | | |
| Ile | Asn | Leu | Glu 100 | Ile | Ser | Ala | Pro | Leu 105 | Thr | Val | Thr | Ser | Glu 110 | Ala | Leu | | | | | |
| Thr | Val | Ala 115 | Ala | Ala | Ala | Pro | Leu 120 | Met | Val | Ala | Gly | Asn 125 | Thr | Leu | Thr | | | | | |
| Met | Gln 130 | Ser | Gln | Ala | Pro | Leu 135 | Thr | Val | His | Asp | Ser 140 | Lys | Leu | Ser | Ile | | | | | |
| Ala 145 | Thr | Gln | Gly | Pro | Leu 150 | Thr | Val | Ser | Glu | Gly 155 | Lys | Leu | Ala | Leu | Gln 160 | | | | | |
| Thr | Ser | Gly | Pro | Leu 165 | Thr | Thr | Thr | Asp | Ser 170 | Ser | Thr | Leu | Thr | Ile 175 | Thr | | | | | |
| Ala | Ser | Pro | Pro 180 | Leu | Thr | Thr | Ala | Thr 185 | Gly | Ser | Leu | Gly | Ile 190 | Asp | Leu | | | | | |
| Lys | Glu | Pro | Ile | Tyr | Thr | Gln | Asn | Gly | Lys | Leu | Gly | Leu | Lys | Tyr | Gly | | | | | |

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

4-31452A.ST25.txt

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
450 455 460

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Asn | Asn | Ser | Phe | Leu | Asp | Pro | Glu | Tyr | Trp | Asn | Phe | Arg |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
515 520 525

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Leu | Thr | Ile | Thr | Leu | Asn | Gly | Thr | Gln | Glu | Thr | Gly | Asp | Thr |
| 530 | | | | | | 535 | | | | | 540 | | | | |

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
565 570 575

Ile Ala Gln Glu

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
 76
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
 24
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
 72
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
 20
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
 68
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
 16
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
 64
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

09870200.050001

4-31452A.ST25.txt

| | | | | | | | |
|---|----|-----|--|-----|--|-----|--|
| 385 | | 390 | | 395 | | 400 | |
| ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag | 12 | | | | | | |
| 48 | | | | | | | |
| Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu | | | | | | | |
| | | 405 | | 410 | | 415 | |
| aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata | 12 | | | | | | |
| 96 | | | | | | | |
| Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile | | | | | | | |
| | | 420 | | 425 | | 430 | |
| ctt gct aca gtt tca gtt ttg gct gct gca ggc agt ttg gct cca ata | 13 | | | | | | |
| 44 | | | | | | | |
| Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile | | | | | | | |
| | | 435 | | 440 | | 445 | |
| tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat | 13 | | | | | | |
| 92 | | | | | | | |
| Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn | | | | | | | |
| | | 450 | | 455 | | 460 | |
| gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt | 14 | | | | | | |
| 40 | | | | | | | |
| Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe | | | | | | | |
| | | 465 | | 470 | | 475 | |
| aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga | 14 | | | | | | |
| 88 | | | | | | | |
| Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly | | | | | | | |
| | | 485 | | 490 | | 495 | |
| ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc | 15 | | | | | | |
| 36 | | | | | | | |
| Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala | | | | | | | |

4-31452A.ST25.txt

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa 17
46
Tyr Ile Ala Gln Glu

580

<210> 14
<211> 581
<212> PRT
<213> Artificial

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

09870203 053001

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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
      20              25              30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
      35              40              45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50              55              60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
      65              70              75              80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
      85              90              95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
      100              105              110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
      115              120              125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
      130              135              140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
      145              150              155              160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
      165              170              175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
      180              185              190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

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195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

390

395

400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

| | | | | | | | | | | | | | | | | |
|---|-----|-----|--|--|--|-----|--|-----|--|--|--|--|-----|-----|--|-----|
| gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 76 | | | | | | | | | | | | | | | | 5 |
| Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu | | | | | | | | | | | | | | | | |
| | 180 | | | | | 185 | | | | | | | 190 | | | |
| aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 24 | | | | | | | | | | | | | | | | 6 |
| Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly | | | | | | | | | | | | | | | | |
| | 195 | | | | | 200 | | | | | | | 205 | | | |
| gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 72 | | | | | | | | | | | | | | | | 6 |
| Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr | | | | | | | | | | | | | | | | |
| | 210 | | | | | 215 | | | | | | | 220 | | | |
| ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 20 | | | | | | | | | | | | | | | | 7 |
| Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr | | | | | | | | | | | | | | | | |
| | 225 | | | | | 230 | | | | | | | 235 | | | 240 |
| gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 68 | | | | | | | | | | | | | | | | 7 |
| Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala | | | | | | | | | | | | | | | | |
| | | 245 | | | | | | 250 | | | | | | 255 | | |
| gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 16 | | | | | | | | | | | | | | | | 8 |
| Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val | | | | | | | | | | | | | | | | |
| | | 260 | | | | | | 265 | | | | | | 270 | | |
| agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 64 | | | | | | | | | | | | | | | | 8 |
| Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln | | | | | | | | | | | | | | | | |
| | | 275 | | | | | | 280 | | | | | | 285 | | |

4-31452A.ST25.txt

| | | |
|---|-----|---------|
| ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 | | 9 |
| Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn | | |
| 290 | 295 | 300 |
| aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 | | 9 |
| Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu | | |
| 305 | 310 | 315 320 |
| gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 | | 10 |
| Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile | | |
| 325 | 330 | 335 |
| gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 | | 10 |
| Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro | | |
| 340 | 345 | 350 |
| aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04 | | 11 |
| Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp | | |
| 355 | 360 | 365 |
| tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 52 | | 11 |
| Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp | | |
| 370 | 375 | 380 |
| agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 00 | | 12 |
| Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr | | |

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

tac att gcc caa gaa taa 17
46
Tyr Ile Ala Gln Glu

| | |
|-------|------------|
| <210> | 16 |
| <211> | 581 |
| <212> | PRT |
| <213> | Artificial |

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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
      20              25              30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
      35              40              45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50              55              60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
      65              70              75              80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
      85              90              95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
      100              105              110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
      115              120              125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
      130              135              140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
      145              150              155              160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
      165              170              175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
      180              185              190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

```

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
565 570 575

Tyr Ile Ala Gln Glu

580

<210> 17
 <211> 1740
 <212> DNA
 <213> Artificial

<220>

<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted

<220>

<221> CDS

<222> (1)..(1740)

<400> 17

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct
 44

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc
 92

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

| | | | |
|----|----|----|----|
| 65 | 70 | 75 | 80 |
|----|----|----|----|

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2
88

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3
36

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3
84

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4
32

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4
80

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5
28

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5
76

180

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6
24

195

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6
72

210

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7
20

225

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7
68

245

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8
16

260

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8
64

275

09070200 053000
T00E50 00204000

4-31452A.ST25.txt

| | | | | | | | |
|---|----|-----|--|-----|--|-----|-----|
| 385 | | 390 | | 395 | | 400 | |
| ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag | 12 | | | | | | |
| 48 | | | | | | | |
| Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu | | | | | | | |
| | | 405 | | 410 | | 415 | |
| aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata | 12 | | | | | | |
| 96 | | | | | | | |
| Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile | | | | | | | |
| | | 420 | | 425 | | 430 | |
| ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata | 13 | | | | | | |
| 44 | | | | | | | |
| Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile | | | | | | | |
| | | 435 | | 440 | | 445 | |
| tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat | 13 | | | | | | |
| 92 | | | | | | | |
| Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn | | | | | | | |
| | | 450 | | 455 | | 460 | |
| gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt | 14 | | | | | | |
| 40 | | | | | | | |
| Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe | | | | | | | |
| | | 465 | | 470 | | 475 | 480 |
| aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga | 14 | | | | | | |
| 88 | | | | | | | |
| Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly | | | | | | | |
| | | 485 | | 490 | | 495 | |
| ttt atg cct aac cta tca gct tat cca aaa tct cac act gcc aaa agt | 15 | | | | | | |
| 36 | | | | | | | |
| Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser | | | | | | | |

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15
 84
 Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16
 32
 Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16
 80
 Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17
 28
 Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa 17
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 Ala Gln Glu

<210> 18
 <211> 579
 <212> PRT
 <213> Artificial

<400> 18

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

Page 79

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

4-31452A.ST25.txt

385 390 395 400

390

395

400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2
40

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

165 170 175

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
290 295 300

ggt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
325 330 335

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
355 360 365

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15
36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

510

515 520 525

530 535 540

545 550 555 560

565 570 575

<400> 20

Page 87

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

F00250 2020/05/04

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

4-31452A.ST25.txt

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
565 570 575

Ala Gln Glu

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<220>
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<220>
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<222> (1)..(38)

<400> 21
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<210> 22
<211> 38
<212> DNA
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<220>
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<220>
<221> primer_bind
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<400> 22
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38

<210> 23
<211> 38
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<220>
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38
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|-------|------------|
| <210> | 24 |
| <211> | 38 |
| <212> | DNA |
| <213> | Artificial |

<220>
<223> PCR primer

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<220>
<221> primer_bind
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38
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| | |
|-------|------------|
| <210> | 25 |
| <211> | 36 |
| <212> | DNA |
| <213> | Artificial |

<220>
<223> PCR primer

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<220>
<221> primer_bind
<222> (1) .. (36)
```

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36
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| | |
|-------|------------|
| <210> | 26 |
| <211> | 36 |
| <212> | DNA |
| <213> | Artificial |

<220>
<223> PCR primer

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<220>
<221> primer_bind
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<211> 36
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<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)

<400> 27
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<210> 28
<211> 36
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<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)

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tattggagcc aaactgccaa cagccaaaac tgaaac
36

<210> 29
<211> 36
<212> DNA
<213> Artificial

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4-31452A.ST25.txt

$\langle 220 \rangle$

<223> PCR primer

<220>

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<221> primer_bind
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$$\langle 222 \rangle \quad (1) \dots (\bar{3}6)$$

<400> 29

gtttcagttt tggctgctgc aggcagtttg gctcca

36

<210> 30

<211> 36

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> primer bind

$$\langle 222 \rangle \quad (1) \dots (\bar{3}6)$$

<400> 30

tggagccaaa ctgcctgcag cagccaaaac tgaaac

36

<210> 31

<211> 36

<212> DNA

<213> Artificial

$\langle 220 \rangle$

<223> PCR primer

$\langle 220 \rangle$

<221> primer bind

$$\langle 222 \rangle \quad (1) \dots (\bar{3}6)$$

<400> 31

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36

<210> 32

<211> 36

<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
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<222> (1)..(36)

<400> 32
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36

<210> 33
<211> 39
<212> DNA
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<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(39)

<400> 33
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39

<210> 34
<211> 39
<212> DNA
<213> Artificial

<220>
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<220>
<221> primer_bind
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39

<222> (1)..(33)

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33

<210> 41

<211> 33

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(33)

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33

<210> 42

<211> 32

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<220>

<221> primer_bind

<222> (1)..(32)

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32

<210> 43

<211> 10

<212> PRT

<213> Artificial

<220>

<223> cRGD consensus sequence

4-31452A.ST25.txt

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His Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5 10

09870203.053001
T00E50" C0204860